

GenCore version 4.5  
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## OM nucleic - nucleic search, using sw model

Run on: June 29, 2002, 22:06:22 ; Search time 17398.4 seconds  
(without alignments)  
1042.620 Million cell updates/sec

Title: US-09-303-518D-131

Perfect score: 1344

Sequence: 1 atgattaaatcaaaaaagg.....ccattgagaagaagcgtga 1344

Scoring table: IDENTITY\_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:\*  
1: em\_estba:\*  
2: em\_estba:\*  
3: em\_estba:\*  
4: em\_estba:\*  
5: em\_estba:\*  
6: em\_estba:\*  
7: em\_estba:\*  
8: em\_estba:\*  
9: em\_estba:\*  
10: em\_estba:\*  
11: em\_estba:\*  
12: em\_estba:\*  
13: em\_estba:\*  
14: em\_estba:\*  
15: em\_estba:\*  
16: em\_estba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	110.2	8.2	349	12	CNS07GYI
2	39.2	2.9	528	10	BG606950
3	38.6	2.9	458	9	AW714071
4	38.2	2.8	407	9	AW712028
5	38.2	2.8	684	10	B1728886
6	38	2.8	384	9	AI392198
7	37.4	2.8	434	10	BG578214
8	37.4	2.8	621	10	BMA90565
9	37.2	2.8	320	9	AV938950
10	37.2	2.8	376	10	BF293584
11	37.2	2.8	577	9	AV938949
12	37	2.8	378	10	D47749
13	37	2.8	497	12	P947R
14	36.8	2.7	606	9	AA538611
15	36.6	2.7	632	10	BE775370
16	36.6	2.7	890	10	B1949615
17	36.4	2.7	216	10	BE360609

18	36.2	2.7	328	10	BE424405
19	36.2	2.7	407	10	BF428970
20	36.2	2.7	460	10	BG262553
21	36.2	2.7	460	10	BE590713
22	36.2	2.7	475	10	BE775489
23	36.2	2.7	505	9	AA614629
24	36.2	2.7	578	9	AL508674
25	36.2	2.7	595	10	B1479848
26	36.2	2.7	625	10	BE590921
27	36.2	2.7	639	10	BG650187
28	36.2	2.7	893	9	AL523270
29	36.2	2.7	921	10	B1147211
30	36.2	2.7	943	9	AL556080
31	36	2.7	349	9	AJ282139
32	36	2.7	357	9	AJ282150
33	35.8	2.7	321	12	AG966942
34	35.8	2.7	574	10	B1949252
35	35.8	2.7	615	10	BG579193
36	35.8	2.7	630	10	BG521603
37	35.6	2.6	152	10	BF769109
38	35.6	2.6	344	10	C26554
39	35.6	2.6	394	12	A2049430
40	35.6	2.6	506	9	AL399239
41	35.6	2.6	779	10	B1464724
42	35.4	2.6	336	10	D47324
43	35.4	2.6	613	10	BG577607
44	35.2	2.6	580	10	BG262171
45	35.2	2.6	687	12	AG184405
46	35.2	2.6	323	9	AL368671
47	35	2.6	361	10	BE776874
48	35	2.6	364	10	BE285901
49	35	2.6	433	9	AM238848
50	35	2.6	497	10	BE378302
51	35	2.6	501	10	BE396602
52	35	2.6	525	10	BE407307
53	35	2.6	554	10	BE792826
54	35	2.6	582	10	BM042302
55	35	2.6	605	10	B1195835
56	35	2.6	605	10	BE907017
57	35	2.6	624	10	BE394122
58	35	2.6	627	10	BE302953
59	35	2.6	636	10	BE255207
60	35	2.6	659	10	BE254129
61	35	2.6	671	10	BE794312
62	35	2.6	676	10	BM042451
63	35	2.6	683	10	BM006767
64	35	2.6	686	10	BG618861
65	35	2.6	691	10	BG469125
66	35	2.6	721	10	BE299424
67	35	2.6	727	10	BE612759
68	35	2.6	733	10	BG165939
69	35	2.6	762	10	B1161016
70	35	2.6	764	10	BG481496
71	35	2.6	766	9	AL527125
72	35	2.6	768	9	AL559560
73	35	2.6	772	10	BG760541
74	35	2.6	775	10	BG397732
75	35	2.6	777	10	BG470987
76	35	2.6	779	9	AL538949
77	35	2.6	779	10	BG575348
78	35	2.6	779	10	BG756437
79	35	2.6	787	9	AL558662
80	35	2.6	793	10	BG473919
81	35	2.6	794	10	BG743980
82	35	2.6	793	10	AL528918
83	35	2.6	816	10	BE204556
84	35	2.6	827	10	BG251414
85	35	2.6	829	10	BM453887
86	35	2.6	836	9	AL521335
87	35	2.6	839	9	BG283881
88	35	2.6	850	10	BE882034
89	35	2.6	867	10	BE901896
90	35	2.6	872	10	BE797780

BE424405	WHE078_E
BF428970	WHE171_E
BG262553	WHE0937_D
BE590713	WHE0856_A
BE775489	MY-01-E-0
AA614629	np54B11_S
AL508674	AL508674
B1479848	WHE3452_G
BE590921	WHE0870_E
BG650187	WHE2328_F
AL523270	AL523270
B1147211	602913119
AL556080	AL556080
AJ282139	4A3A-AAP-
AJ282150	4A3A-AAP-
AG966942	LEIRIN24TR
B1949252	HEMEL1001
BG579193	d424f02.Y
BG521603	12-34_Ste
BF769109	OV3-IT000
C26554	C26554
A2049430	GSSBRU098
AL399239	NCM10F2T3
B1464724	603202344
D47324	R1CS12625A
BG577607	TM_d08D
BG262171	WHE0871_G
AG184405	Pan Trogl
AL368671	qy61h02.X
BE776874	MY-21-H-0
BE285901	EST450492
AM238848	x29f02.Y
BE378302	601236336
BE396602	601288849
BE407307	601301064
BE792826	601584823
BM042302	603616381
BM042451	602749356
B1195835	602749356
BE907017	601499836
BE394122	601311607
BE302953	601157575
BE255207	601113992
BE254129	601113992
BE794312	601591447
BM042451	603616281
BM006767	603616591
BG618861	602718068
BG469125	602511078
BE299424	601118749
BE612759	601452328
BG165939	602344259
B1161016	602865226
BG481496	602528880
AL527125	AL527125
AL559560	AL559560
BG760541	602716979
BG397732	602438793
BG470987	602511964
AL538949	AL538949
BG575348	602597819
BG756437	602715767
AL558662	AL558662
BG473919	602516384
BE743980	602722752
AL528918	AL528918
BE204556	601868165
BG251414	602364061
BM453887	ACENICOURT
AL521335	AL521335
BE283881	602407619
BE882034	601505320
BE901896	601675114
BE797780	602257543

91	35	2.6	892	10	B1836975	B1836975	603084506
92	35	2.6	892	10	B2533873	B2533873	6011128448
93	35	2.6	903	10	B6682741	B6682741	6026512228
94	35	2.6	904	10	B6032362	B6032362	602301345
95	35	2.6	908	9	AL526515	AL526515	6026515
96	35	2.6	919	10	B1858840	B1858840	603388757
97	35	2.6	962	10	BG340804	BG340804	602462411
98	35	2.6	964	9	AL561126	AL561126	AL561126
99	35	2.6	975	10	B2733018	B2733018	6015695003
100	35	2.6	976	10	BM451205	BM451205	AGENCOCURT

## ALIGNMENTS

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RESULT 1
CNS07GY1
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
1. 349
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="23104"
/clone_lib="Notredame1"
/note_end : 177
2 a 100 c 106 g 71 t

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Best Local Similarity	59.4%	Pred No. 3.3e-20		
Matches 187	Conservative 0	Mismatches 128	Indels 0	Gaps 0
QY	629	atgaatttggcggccgcacatcctgcgcggttaagtgcacgacattcatcattcgcagc	688	
Db	32	ATGAGTTTGCTGTCGCCGCATCCGGCGGGTCTGTGGCGGACGCACATCCATTTCCTTGAC	91	
QY	689	cagtcggcgcggaataaaccgctgtgacatcataattataagaacgtatgtctatgcagc	748	
Db	92	CGGTAGGCTGCACAAAACAGGTCTGGCATCTTAATTATATGAGACGTCATCGGCATCGGTA	151	
QY	749	gtttgttcgaacagcgcgctgaatatacgaagcgcgtgtgttccttgcgtgcgcgaag	808	
Db	152	CGCTTTCACATCCCGAGAGCTGTGCGCGGAGACGATCATCCCATTCGTGGGCGCGAG	211	
QY	809	tcaacaacacgcgcctcttgcgtaccgctttgtgtgcgaagtgctcctaactlaccgcgcg	868	

[illegible]

RESULT 2  
PC6060E0

JOURNAL	TITLE
COMMENT	
FEATURES	REFERENCE
source	AUTHORS
	ORGANISM
	SOURCE
	ACCESSION
	VERSION
	KEYWORDS
	DEFINITION
	DCCOS
	B6G06930
	WHE2492_E05_110ZS Trifolium monocoecum early reproductive apex cDNA library Trifolium monocoecum cDNA clone WHE2492_E05_110, mRNA sequence.
	B6G06930
	B6G06930.1 GI:13656933
	EST.
	Trifolium monocoecum.
	Trifolium monocoecum
	Euarystia Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triliceae; Triticum .
	1 (bases 1 to 528)
	C., Anderson,O.P., Chao,S., Dubcovsky,J., Echenique,Y., Han,P.S., Hsia ,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L., Stamova,B. and Tong,J.C.
	The Structure and function of the expressed portion of the wheat genomes - Early reproductive apex cDNA library from Triticum monocoecum
	Unpublished (2001)
	Contact: Olin Anderson
	US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
	800 Buchanan Street, Albany, CA 94710, USA
	Tel.: 5105595773
	Fax: 5105595818
	Email: oanderson@pw.usda.gov
	Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
	Seq primer: Stratagene SK primer.
	Location/Qualifiers
	I..528

```

FEATURES
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        1..528
            Location/Qualifiers
                /organism="Triticum monococcum"
                /cultivar="DV92"
                /db_xref="taxon:4568"
                /clone="WHE2492_E05_110"
                /clone_11b="Triticum monococcum early reproductive apex
                cDNA library"
                /tissue_type="Early reproductive apex"
                /dev_stage="Seven week-old plants"
                /lab_host="E. coli XL0LR"
                /note="Vector: Lambda uni-ZAP XR, excised phagemid;
                Site_1: EcoRI; Site_2: XhoI; The tissue, total RNA, and
                poly(A) RNA were prepared from apex at double-ridge stage
                to terminal-spikelet stage during transition from
                vegetative state to flower state, a cDNA library was made,
                and the cDNA libraries were in vivo excised at the
                University of California, Davis (V. Echenique, B. Stamova
                , J. Dubcovsky). Plasmid DNA preparations and DNA
                sequencing were performed in the OD Anderson lab (all
                other authors)."
BASE COUNT
    45 a      245 c      140 g      98 t
ORIGIN

```

Query Match	2.98;	Score 39.2;	DB 10;	Length 528;
Best Local Similarity	50.08;	Pred. No. 4.3;		
Matches 98;	Conservative 0;	Mismatches 98;	Indels 0;	Gaps 0;







AUTHORS	Sato,K., Saisno,D. and Takeda, K.
TITLE	Barley EST sequencing project in NIG and Okayama Univ
JOURNAL	Unpublished (2002)
COMMENT	Contact: Tadasi Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshin@genes.nig.ac.jp.
FEATURES	location/Qualifiers
source	1..320 /organism="Hordeum vulgare subsp. spontaneum" /strain="H602" /db_xref="taxon:77009" /clone="bah20a24" /clone_1ib="K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves" /tissue_type="top three leaves" /dev_stage="adult, heading stage"
BASE COUNT	44 a 113 c 99 g 64 t
ORIGIN	
Query Match	2.8%; Score 37.2; DB 9; Length 320;
Best Local Similarity	72.7%; Pred. No. 12;
Matches	48; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
Oy	437 cgctgcacatcgttcgatggagaccacccgctgcgcgcgcacccacgtca 496
Db	218 CGTCAGCAGATGTTCTCTCACGGCGATGGCCAAACCGCTTGCCCAACCTCAGCGTCA 277
Oy	497 tcacca 502
Db	278 GCACCA 283
RESULT 10	
LOCUS	BF293584 376 bp mRNA linear EST 17-NOV-2000
DEFINITION	WHE2158.E09.J18Z5 Triticum turgidum L. var. durum (durum wheat) whole plant cDNA library Triticum turgidum cDNA clone
ACCESSION	WHE2158.E09.J18, mRNA sequence.
VERSION	BF293584
KEYWORDS	EST.
SOURCE	BF293584.1 GI:11224648
ORGANISM	Triticum turgidum. Triticum turgidum. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Triticum.
REFERENCE	1 (bases 1 to 376) Akhunov,E., Anderson,O.D., Chao,S., Chin,A., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Kianlan,P., Iazo,G.R., Miller,R., Otto,C., Rausch,C.J., Seaton,C.L., Simons,K., Tong,J.C. and Zhang,D. The structure and function of the expressed portion of the wheat genomes - Whole plant cDNA library from Triticum turgidum L. var. durum
TITLE	Unpublished (2000)
JOURNAL	Contact: Olin Anderson
COMMENT	US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 510595773 Fax: 510595818 Email: anderso@w.usda.gov Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratiene SK primer. Location/Qualifiers
FEATURES	1..376 /organism="Triticum turgidum" /strain="H602"

AUTHORS	/cultivar="Langdon-16"
TITLE	/db_xref="taxon:4571"
JOURNAL	/clone="WHE2158.E09.J18"
COMMENT	/clone_1ib="Triticum turgidum L. var. durum (durum wheat) whole plant cDNA library" /tissue_type="All tissues" /dev_stage="Different growth stages" /lab_host="E. coli SOLR" /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; Plants were grown in a growth chamber at North Dakota State University (Kianlan, Otto, Simons). Tissues collected from seven-day etiolated seedling leaf, stem, root and seed; leaf from plant at fourth leaf stage; spike from pre-anthesis through 20 days after anthesis; flag leaf; leaf and stem tissue from tillers, and root. Total RNA and poly(A) RNA were prepared from each tissue and then pooled. A cDNA library was made, and the cDNA clones were in vivo excised to give Bluescript phagemids in the TJ Close lab (Akhunov, Chin, Choi, Close, Fenton, Kianlan, Otto, Simons, Zhang) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
BASE COUNT	37 a 154 c 136 g 49 t
ORIGIN	
Query Match	2.8%; Score 37.2; DB 10; Length 376;
Best Local Similarity	55.4%; Pred. No. 13;
Matches	72; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
Oy	1197 cgtcgcgatcacgcagcgcgacggttggtgcttggaattgacaagaagacct 1256
Db	57 CCGGCACGAGGCCGGGGCGGAGGTGCGCTGACTGGCGGTGAGAGACGT 116
Oy	1257 cgctttgcaagtctgtctgccgggcaaatagatacgcgcgcttgccaagt 1316
Db	117 CGCCGACGACGCGGTTCGCTCGGGCGCGCGGCGAGAGCGCGTGGCGCGCT 176
Oy	1317 gctgaaac 1326
Db	177 GCTCAGAGC 186
RESULT 11	
LOCUS	AV938949 577 bp mRNA linear EST 18-JAN-2002
DEFINITION	AV938949 K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves Hordeum vulgare subsp. spontaneum cDNA clone bah20a23 5', mRNA sequence.
ACCESSION	AV938949
VERSION	AV938949.1 GI:18234746
KEYWORDS	EST.
SOURCE	Hordeum vulgare subsp. spontaneum. Hordeum vulgare subsp. spontaneum.
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE	1 (bases 1 to 577) Sato,K., Saisno,D. and Takeda, K. Barley EST sequencing project in NIG and Okayama Univ
TITLE	Unpublished (2002)
JOURNAL	Contact: Tadasi Shin-i
COMMENT	Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshin@genes.nig.ac.jp.
FEATURES	location/Qualifiers
source	1..577 /organism="Hordeum vulgare subsp. spontaneum" /strain="H602"







/db\_xref="taxon:4513"  
 /clone="HVSME10014016f"  
 /clone\_lib="Hordeum vulgare spike EST library HVCNNA0012  
 (Fusarium infected)"  
 /tissue\_type="Spike"  
 /lab\_host="TJCI21"  
 /note="vector: pbluescript SK(-); Site1: EcoRI; Site2:  
 XhoI; Plants were grown at the University of Minnesota in  
 the GJ Muehlbauer lab; spikes were harvested and snap  
 frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium  
 graminearum inoculation (Heinen). In the TJ Close lab at  
 the University of California, Riverside, total RNA was  
 prepared from each sample pool, equal quantities of all  
 eight RNA pools were combined, poly(A) RNA was purified  
 from the mixture, one primary unamplified cDNA library was  
 made, and 1 million pfu were in vivo excised to give  
 pbluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi  
 ). Phagemids were plated and picked at the Clemson  
 University Genomics Institute (CUGI) (Begum, Palmer,  
 Frisch, Atkins and Wing). Plasmid DNA preparations, DNA  
 sequencing and sequence analysis were performed at CUGI  
 (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).  
 The sequence has been trimmed to remove vector sequence  
 and contains a minimum of 100 bases of phred value 20 or  
 above. For more details on library preparation and  
 sequence analysis see  
 http://www.genome.clemson.edu/projects/barley. To order  
 this clone see http://www.genome.clemson.edu/orders Also  
 see Close TJ, Wing R, Kleinhoft A, Wise R (2001)  
 Genetically and physically anchored EST resources for  
 barley genomics. Barley Genetics Newsletter 31:29-30.  
 (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 188 a 293 c 204 g 202 t 1 others

Query Match 2.7%; Score 36.6; DB 10; Length 890;  
 Best Local Similarity 52.3%; Pred. No. 29;  
 Matches 81; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 961 cacaatcagattccgtatcgaagaagccgagcaagaagctgttcggtggtg 1020  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 265 CTCACACCCGGTGGCGCTTCGAGAACCCCGCAAGAGAGCTCGCGCTGTCGCC 324  
 Qy 1021 ccgagccgagcaaaactcatcagcgacacactctggtccatttcctaaanaaaa 1080  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 325 ACCAACACCGGACGAGCGCTTCGAGACCCCTTCGCTTCGATGCGATATCATCTGC 384  
 Qy 1081 ctctcaagttcagacagccgtcaagcgagcga 1115  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 385 CACCGCGGCGCCGAGAACCGCGTCAAGTCCGCCAA 419

RESULT 17  
 BE360609/c 216 bp mRNA linear EST 20-JUL-2000  
 LOCUS DGL\_64\_H11.g1\_A002 Dark Grown 1 (DGL) Sorghum bicolor CDNA, mRNA  
 DEFINITION sequence.  
 accession BE360609  
 version BE360609.1 GI:9302166  
 keywords EST.  
 source sorghum.  
 organism Sorghum bicolor

REFERENCE  
 AUTHORS Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 216)  
 Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt  
 L. H.

TITLE An EST database from Sorghum: dark-grown seedlings  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Cordonnier-Pratt MM  
 Department of Botany

The University of Georgia  
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
 Tel: 706 542 1860  
 Fax: 706 542 1805  
 Email: mmp@atuga.edu  
 Sequences have been trimmed to exclude polyA, vector and regions  
 below Phred quality 16. The threshold for highest quality sequence  
 is 20.  
 Seq primer: PolyTMix  
 High quality sequence start: 4  
 High quality sequence stop: 207  
 POLYA=Yes.  
 Location/Qualifiers

## FEATURES

source

1..216  
 /organism="Sorghum bicolor"  
 /db\_xref="taxon:4558"  
 /clone\_lib="Dark Grown 1 (DGL)"  
 /note="Organ: 5-day-old dark grown seedlings; Vector:  
 lambda Zap; Site\_1: XhoI; Site\_2: EcoRI; The library was  
 made from poly-A RNA in the cloning vector lambda Zap II.  
 Clones to be sequenced were prepared by mass excision."  
 44 a 70 c 80 g 22 t

Query Match 2.7%; Score 36.4; DB 10; Length 216;  
 Best Local Similarity 51.2%; Pred. No. 17;  
 Matches 85; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy 1036 tactcaatcagcgacacactctggcatttctctaanaaacacttcaagtacg 1095  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 215 TCTCTGATCTTGGGCGAGGCGCTCCCTGCCCGGCTGCTCTCTCATGCGCC 156  
 Qy 1096 acagcgatcagcgagcgacccgagcagctgttacccgacattagcgagtaatg 1155  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 155 GCGCGCGCCATGTGCGCGCCCGCCCTGTGTGACATCTTGGCGATGATGGGTTGACAG 96  
 Qy 1156 ccgttgacatctgactactctgttttgcgagattatogtgcg 1201  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 95 CGACTCGACCTCTTCATCTTCTCGAATCGTCCGCTCGCGG 50

RESULT 18  
 BE424405 328 bp mRNA linear EST 24-JUL-2000  
 LOCUS WHE0078.E09.J1825 wheat endosperm cDNA library Triticum aestivum  
 DEFINITION cDNA clone WHE0078.E09.J18, mRNA sequence.  
 accession BE424405  
 version BE424405.1 GI:9422248  
 keywords EST.  
 source bread wheat.  
 organism Triticum aestivum

REFERENCE  
 AUTHORS Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae  
 ; Triticeae; Triticum.  
 1 (bases 1 to 328)  
 Altenbach, S., Anderson, O.D., Chao, S., Gall, G., Han, P.S., Hsia  
 C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and  
 Tong, J.C.

TITLE The structure and function of the expressed portion of the wheat  
 genomes - Endosperm cDNA library  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Olin Anderson  
 US Department of Agriculture, Agriculture Research Service, Pacific  
 West Area, Western Regional Research Center  
 800 Buchanan Street, Albany, CA 94710, USA  
 Tel: 5105585773  
 Fax: 5105585818  
 Email: oanderson@pw.usda.gov

Sequence have been trimmed to remove vector sequence and low  
 quality sequence with phred score less than 20  
 Seq primer: Stragene SK primer.  
 Location/Qualifiers



















Db 316 TTCCAGCGGAGCGCCGAGCAGCAGCGCCGCCGAGATGAGACACGAGTGT 257  
 Qy 476 tggcgcgcacccctacgtcatcaagaagccgcgaagacttcaacgcgcctgt 535  
 Db 256 TCATTGCGGTCCGACGACGCGTGTGTGACGAGCCGAGCGCGGCGGCGC 197  
 Qy 536 tggattagccgcctgacgca 558  
 Db 196 TTGAAGCTGATAGCGCGCGCGA 174

# RESULT 34

Bi949252 574 bp mRNA linear EST 19-OCT-2001  
 LOCUS HVSME10013A08f Hordeum vulgare spike EST library HVCNDN0012  
 DEFINITION (Fusarium infected) Hordeum vulgare cDNA clone HVSME10013A08f, mRNA

ACCESSION Bi949252  
 VERSION Bi949252  
 KEYWORDS EST.  
 SOURCE Barley.  
 ORGANISM Hordeum vulgare  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 1 (bases 1 to 574)  
 Wing, R., Muehlbauer, G.J., Close, T.J., Kleinbols, A., Wise, R., Heinen  
 S., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T.,  
 Simmons, D., Fenton, R.D., Malatrasi, M., Choi, D.W., Oates, R. and Main  
 D.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Development of a genetically and physically anchored EST resource  
 for barley genomics: Fusarium infected Morex spike cDNA library  
 Unpublished (2001)  
 Contact: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: rwing@clemson.edu

FEATURES  
 SOURCE

Total hg bases = 227  
 Seq primer: AATTAACCTCCTACATTAAGG  
 High quality sequence start: 61  
 High quality sequence stop: 465.  
 Location/Qualifiers

1..574  
 /organism="Hordeum vulgare"  
 /cultivar="Morex"  
 /db\_xref="taxon:4513"  
 /clone="HVSME10013A08f"  
 /clone\_lib="Hordeum vulgare spike EST library HVCNDN0012  
 (Fusarium infected)"  
 /tissue\_type="Spike"  
 /lab\_host="TJC121"  
 /note="Vector: Bluescript SK(-); Site:1: EcoRI; Site:2:  
 XhoI; Plants were grown at the University of Minnesota in  
 the GJ Muehlbauer lab; spikes were harvested and snap  
 frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium  
 graminearum inoculation (Heinen). In the TJC Close lab at  
 the University of California, Riverside, total RNA was  
 prepared from each sample pool, equal quantities of all  
 eight RNA pools were combined, poly(A) RNA was purified  
 from the mixture, one primary unamplified cDNA library was  
 made, and 1 million pfu were in vivo excised to give  
 Bluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi  
 ). Phagemids were plated and picked at the Clemson  
 University Genomics Institute (CUGI) (Begum, Palmer,  
 Frisch, Atkins and Wing). Plasmid DNA preparations, DNA  
 sequencing and sequence analysis were performed at CUGI  
 (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).  
 The sequence has been trimmed to remove vector sequence  
 and contains a minimum of 100 bases of phred value 20 or

above. For more details on library preparation and  
 sequence analysis see  
<http://www.genome.clemson.edu/projects/barley>. To order  
 this clone see <http://www.genome.clemson.edu/orders> Also  
 see Close T.J., Wing R., Kleinbols A., Wise R (2001)  
 Genetically and physically anchored EST resources for  
 barley genomics. Barley Genetics Newsletter 31:29-30.  
 (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"

BASE COUNT 178 a 128 c 137 g 123 t 8 others  
 ORIGIN

Query Match 2.7%; Score 35.8; DB 10; Length 574;  
 Best Local Similarity 49.7%; Pred. No. 40;  
 Matches 88; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

Qy 152 tcaaaaaggccaagtgcgtgttgaagacaaaagaatccggcgtagtattactgcgc 211

Db 214 TCAAGCAGCGGTGACAGGATCTTGATGAAACAAAGCTCTTGGGATACAAAGGNN 273

Qy 212 cggcttcaggcaaatccgcgcgtatccgcgtgcgaagcgctacttcgtcgtcg 271

Db 274 CAACCTCAATCAAGATCTGCGCATTCACCTGCTGTTCAAGCTTCAAGCCATGACGCCG 333

Qy 272 tgaatgcgttgaaggaacgaacgaatcgagctgcagctacgtactgaagcgc 328

Db 334 AGCTCACAGCTGGTGTCTCAACTTACATGATGATGACAGCGATACACCATATGAC 390

RESULT 35  
 Bi949193 615 bp mRNA linear EST 11-APR-2001  
 LOCUS d124f02.y1 Wellcome CRC PRN3 St10.5 Xenopus laevis cDNA clone  
 DEFINITION IMAGE:3558290.5' similar to SW:SF02.CHICK P30352 SPLICING FACTOR,  
 ARGININE/SERINE-RICH 2 ; , mRNA sequence.

ACCESSION Bi949193  
 VERSION Bi949193  
 KEYWORDS EST.  
 SOURCE African clawed frog.  
 ORGANISM Xenopus laevis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 Xenopodinae; Xenopus.  
 1 (bases 1 to 615)  
 Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Page, D.,  
 Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person  
 B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,  
 Waterston, R. and Wilson, R.  
 WashU Xenopus EST project, 1999  
 Unpublished (1999)  
 Contact: Sandy Clifton, Ph.D.  
 WashU Xenopus EST project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 Library constructed by N. Garrett, P. Lemaire, A.M. Zorn, and J.B.  
 Gurdon (Wellcome/CRC Institute). DNA Sequencing by: Washington  
 University Genome Sequencing Center  
 Clone distribution: Xenopus clones from this library are available  
 through the I.M.A.G.E. Consortium/LML at: [info@image.llnl.gov](mailto:info@image.llnl.gov)  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 474.  
 Location/Qualifiers

1..615  
 /organism="Xenopus laevis"  
 /cultivar="Xenopus laevis"  
 /db\_xref="taxon:8355"  
 /clone="IMAGE:3558290"  
 /clone\_lib="Wellcome CRC PRN3 St10.5"  
 /tissue\_type="embryo, stage 10.5"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Vector: pBSRN3; site\_1: NotI; site\_2: EcoRI; CDNAS

FEATURES  
 SOURCE





RESULT 40  
AI399239  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
COMMENT  
FEATURES  
source

AI399239 506 bp mRNA linear EST 08-FEB-1999  
NCM10F273 Westergaards Neurospora crassa cDNA clone W10F2 5', mRNA sequence.  
AI399239 GI:4242324  
EST.  
Neurospora crassa.  
Neurospora crassa  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariales; Sordariaceae; Neurospora.  
1 (bases 1 to 506)  
Nelson, M.A., Kang, S., Braun, E.L., Crawford, M.E., Dolan, P.L.,  
Leonard, P.M., Mitchell, J., Armijo, A.M., Bean, L., Bluyes, E.,  
Cushling, T., Errett, A., Fleharty, M., Gorman, M., Judson, K., Miller, R.,  
Ortega, J., Pavlova, I., Peter, J., Todisco, S., Trujillo, R.,  
Valentine, J., Wells, A., Werner-Washburne, M., Yazzie, S. and Natvig  
D.O.  
Expressed sequences from conidial, mycelial, and sexual stages of  
Neurospora crassa  
Fungal Genet. Biol. 21, 348-363 (1997)  
97435349  
Contact: Natvig, D.O./Nelson, M.A.  
Department of Biology  
University of New Mexico  
Casteretter Hall, Albuquerque, NM 87131, USA  
Tel: 505 277 3411  
Fax: 505 277 0304  
Email: npeb@biology.unm.edu.  
Location/Qualifiers  
1. 506  
/organism="Neurospora crassa"  
/strain="74-OR23-IV A (FESC 2489)"  
/db\_xref="taxon:5141"  
/clone\_1lb="W10F2"  
/clone\_1lb="Westergaards"  
/sex="Mating type A"  
/tissue\_type="unfertilized sexual tissue"  
/dev\_stage="unfertilized sexual stage"  
/lab\_host="E. coli"  
/note="Vector: pBluescript SK (-); Site\_1: EcoRI; Site\_2:  
XhoI; Westergaard's medium (Nitrogen limiting). Floating  
mycelial mats grown at 25C for 36 hours. cDNA  
directionally cloned into pBluescript SK(-) using the  
Uni-ZAP XR vector system (Stratagene, La Jolla, CA)."  
BASE COUNT 105 a 136 c 132 g 129 t 4 others  
ORIGIN

Query Match 2.6%; Score 35.6; DB 9; Length 506;  
Best Local Similarity 48.2%; Pred. No. 43;  
Matches 95; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

OY 100 gaagaatgctggcagcgcctcgatgaatcaagaagcgtagaacaaga 159  
DB 27 GAGGAATGTCGCCCTTCACGCTTCAGTTGATTCGCCAGAGAGGTAAGGCTCCGCTCAAG 86  
OY 160 ggcgaagtgcgtttgaaagacaagaatcccgagcgtatgattactcgccgcgtctca 219  
DB 87 GGGCAATTCGCGCAAGGGGAGAACANCGTCCGCGCCCATGCTCNCGTCGCGCCGATCG 146  
OY 220 ggcgaatcgccgctattacacgttgcgaaagcgctacttcagtcagtcgtgattgcc 279  
DB 147 GCTAGCGGGGCGCTATTCATGCGCCGTTAAGCGCACCGAAGATGCACCATTTGCT 206  
OY 280 gttgaaggaagaagaga 296  
DB 207 GTTAAAGCGAAGAACNA 223

RESULT 41  
BI464724  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

BI464724 779 bp mRNA linear EST 21-AUG-2001  
603202344F1 NIH\_MGC\_97 Homo sapiens cDNA clone IMAGE:5268155 5',  
mRNA sequence.  
BI464724  
BI464724.1 GI:15255367  
EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 779)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Miklos Falckovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki  
Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLNL1676 row: h column: 12  
High quality sequence stop: 343.  
Location/Qualifiers  
1. 779  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_1lb="IMAGE:5268155"  
/clone\_1lb="NIH\_MGC\_97"  
/lab\_host="DH10B"  
/note="Organ: testis; Vector: pBluescript (modified  
pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (gtcgag  
); Oligo-dT primed using primer 5'-TTTTTTTTTTTAA-3',  
size-selected for average insert size 2.2 kb and  
normalized to 10^5. This is a primary library enriched  
for full-length clones and constructed using the  
Cap-trapper method (Carninci, in preparation). Library  
constructed by M. Brownstein (NIH/NHGRI, National  
Institutes of Health). Note: this is a NIH\_MGC library."  
BASE COUNT 200 a 197 c 242 g 140 t  
ORIGIN

Query Match 2.6%; Score 35.6; DB 10; Length 779;  
Best Local Similarity 57.0%; Pred. No. 53;  
Matches 65; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

OY 641 gccgcattccgctgagtgagcagacattcattcatcagcagcgagcgagcga 700  
DB 221 GCCGAATCCGCGCGGTGGGAGTGGCTGCTGATTCGAATCAACGGGCGCTTCGGCGGA 280  
OY 701 ataaacgctgtgacatcaattacaagacgtgactgcatcgagcgtttgt 754  
DB 281 AGACAGCGCTTCGACACCAAGCCGATTCGCCGGGGCTTCCCAAGGGGCTTTGT 334

RESULT 42  
D47324  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

D47324 356 bp mRNA linear EST 02-AUG-1995  
R1CS12626A Rice green shoot Oryza sativa cDNA, mRNA sequence.  
D47324  
D47324.1 GI:701033  
EST.  
Oryza sativa.  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 356)  
Sasaki, T., Miyao, A. and Yamamoto, K.  
Rice cDNA from callus 1995  
Unpublished (1995)  
Contact: Takuji Sasaki  
National Institute of Agrobiological Resources  
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba,  
305-8602, Japan

Location/Qualifiers  
1. .356

45 a	140 c	101 g	65 t	5 others
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ch	2.68;	Score 35.4;	DB 10;	Length 356;
1 Similarity	46.68;	Pred. NO. 42;		
108; Conservative	0;	Mismatches 124;	Indels 0;	Gaps 0

gagcagaagaagctgttctgctggttgcgcgacgcgacaaactcatcaagcg 1049  
 |||||  
 agctccggtagactcggnccggcgaggcacacacgcggccgacgctggttgcgtccgag 115

CCGGCAGTGGGCACCTTCCTCAATTTCTCCGCTTCATTGGGCGGTGTGCGGCCACGA 175

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CCGCCCTCTTAAGGACATATCCGACGCTCGCCGCGCTGACTTCGACCTG 287

BG577607	613 bp	mRNA	linear	EST 11-APR-2001
Tm_ad_08D07-SKPL Trichuris muris			(parasitic nematode)	mixed adult
Trichuris muris cDNA clone Tm_ad_08D07 5'				mRNA sequence.
C577607				

Trichuris muris.  
Trichuris muris.  
EST.  
BG577607.1 GI:13592671

Ecnatozoa; Metazoa; Nematoda; Enopleia; Trichocephalida; Trichuridae  
Trichuris.  
1 (bases 1 to 613)  
Blaxter, M.L., Parkinson, J., Whittom, C., Daub, J., Guillano, D., Hall

Edinburgh University/Sanger Centre Nematode EST Project  
Unpublished (2000)  
Contact: Blaxter ML  
Institute of Cell Animal and Developmental Biology

University of Edinburgh  
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9  
3JT, UK.  
Tel: +44 131 650 6760

Email: mark.dilxter@ed.ac.uk  
The library was prepared by Richard Grencis, Manchester University, Manchester.  
Sequencing was performed by the Pathogen Sequencing Unit, Sanger Centre, Cambridge, UK (Neil Hall, Mike Quail & Bart Barrell). The sequence contained a Polya tail (trimmed)  
PCR Primers

```

FORWARD: T3
BACKWARD: TTPL
Plate: 08   row: D   column: 07
Seq primer: SKPL
High quality sequence stop: 536
location/Qualifiers
1..613

```

```

/organism="Trichuris muris"
/db_xref="taxon:70415"
/clone="Tm_ad_08p07"
/clone_lib="Trichuris muris (parasitic nematode) mixed
adult"

```

/seq -m160  
 /dev\_stage="adult"  
 /note="Vector: Lambda Zap II; Site: 1: EcoRI (5'end);  
 Site: 2: XhoI (3'end); Trichuris muris is a nematode  
 parasite of rodents related to the human whipworm  
 Trichuris trichiura. The library was constructed from  
 Trichuris muris adults (Edinburgh 'E' strain) maintained  
 in mice, and was provided by Dr. Richard Grencis,  
 University of Manchester."

ch	2.68;	Score 35.4;	DB 10;	Length 613;
1 Similarity	56.48;	Pred. No. 54;		
66; Conservative	0;	Mismatches 51;	Indels 0;	Gaps 0

ccgttcgcctcagcaaaatccctgcccgttagatgcgagccgttcgcacattcgatactg 457  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
taccggtgcctcagccgaccattggagtatatcttttggttcggtgccattcttgcatactg 186

ATGACACGAAGCCTCTGTGC AAAAGCTTCCGTTTC CAGCAGAAACTTCG

580 bp mRNA linear EST 16-FEB-2001  
BG262171  
WHE0871.G02.M03S Wheat 20-45 DAP spike CDNA library Triticum  
aestivum CDNA clone WHE0871.G02.M03, mRNA sequence.

BR262171.1 GI:12863317  
EST.  
bread wheat.  
Triticum aestivum

Euarystota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
; Triticeae; Triticum.  
1 (bases 1 to 580)

P. S., Hsia, C. C., Kang, Y., Lazo, G. R., Miller, R., Rausch, C. J., Seaton, C. L. and Tong, J. C.

Unpublished (2000)  
Contact: Olin Anderson  
Department of Agriculture, Agriculture Research Service, Pacific  
West Area, Western Regional Research Center

800 Buchanan Street, Albany, CA 94710, USA  
Tel: 5105595773  
Fax: 5105595818  
Email: candern@pw.usda.gov

```

quality sequence with phred score less than 20
Seq primer: Stratiogene SK primer.
location/Qualifiers
    1..560
        /organism="Tritium aestivum"
        /cultivar="Chinese Spring"
        /db_xref="taxon:4565"

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```

/clone="WHE0871.G02.M03"
/clone_lib="Wheat 20-45 DAP spike cDNA library"
/tissue_type="Spike and seed"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/notes="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcorI; Site_2: XhoI; Plants were grown in the
greenhouse. Spikes at 20 DAP and seeds at 30 to 45 DAP
were harvested, total RNA and poly(A) RNA were prepared, a
cDNA library was made, and the cDNA clones were in vivo
excised to give Bluescript phagemids in the TJ Clonase Lab
(Choi, Clonase, Fenton) at the University of California,
Riverside. Plasmid DNA preparations and DNA sequencing
were performed in the OD Anderson lab (all other authors
)."
BASE COUNT      157 a      147 c      149 g      126 t      1 others
ORIGIN

```

```

Query Match      2.6%; Score 35.2; DB 10; Length 580;
Best Local Similarity 49.7%; Pred. NO. 60;
Matches 88; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

```

```

QY 152 tcaaaaagcccaagtcgtgttgagacaaaagatccgagctagctatctgcgc 211
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 311 tcaacatggtgacacagatcttgacgacgacacacacacacacacacacac 370
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 212 cggcttcagcaaatccgcgtatccacgctgacgacgacgacgacgacgacg 271
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 371 aactggcattcaaatctctgacattcactgctgacacacacacacacacac 430
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 272 tgaatgcgttgaaagcagcagcaatccagcttcgaacgctacgctgaagcgc 328
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 431 aggtcacacagctggtactacacacacacacacacacacacacacacacac 487
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

## RESULT 45

AG184405

LOCUS AG184405 687 bp DNA linear GSS 09-JAN-2002  
 DEFINITION Pan troglodytes DNA, clone: RP43-058C22.T7, genomic survey  
 sequence.

ACCESSION AG184405

VERSION AG184405.1 GI:16714085

KEYWORDS GSS; GSS (genome survey sequence);

SOURCE Pan troglodytes male lymphocytes DNA, clone\_lib:RPCI-43 Chimpanzee  
 Male BAC library clone:RP43-058C22.T7.

ORGANISM

Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE

1 (sites)  
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
 Totoki, Y., Watanabe, H. and Sakaki, Y.

TITLE

BAC end sequences of library RPCI-43  
 Unpublished

JOURNAL

2 (bases 1 to 687)  
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
 Totoki, Y., Watanabe, H. and Sakaki, Y.

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

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AUTHORS

source

```

1. 687
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-058C22.T7"
/sex="male"
/clone_lib="RPCI-43 Chimpanzee Male BAC library"
BASE COUNT      138 a      211 c      164 g      174 t
ORIGIN

```

```

Query Match      2.6%; Score 35.2; DB 12; Length 687;
Best Local Similarity 53.7%; Pred. NO. 65;
Matches 73; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

```

```

QY 1035 atactcaccacgacgacacacacacacacacacacacacacacacacac 1094
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 374 atgttcaggacccagacacacacacacacacacacacacacacacacacac 433
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1095 gacagccgtaaacgagcgcgacacacacacacacacacacacacacacac 1154
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 434 gttaggagagacgacgacgacacacacacacacacacacacacacacacac 493
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1155 gccgttggacacacacacacacacacacacacacacacacacacacacac 1170
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 494 gcccttcacacacacacacacacacacacacacacacacacacacacacac 509
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Search completed: June 29, 2002, 22:06:44  
 Job time: 1757 sec